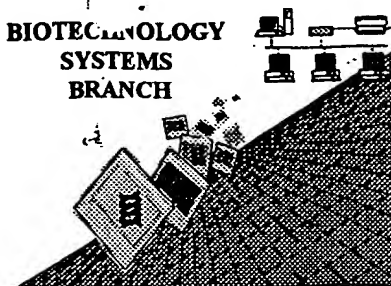


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/914,220

Source:

P5/09

Date Processed by STIC:

9/14/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/914,220

DATE: 09/14/2001

TIME: 10:39:35

Input Set : A:\Debelseq.txt

Output Set: N:\CRF3\09142001\I914220.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Schulz Dr., Burkhard
 5 <120> TITLE OF INVENTION: DNA sequence of a protein that is similar to FKBP
 7 <130> FILE REFERENCE: SCU-001 PCT
 9 <140> CURRENT APPLICATION NUMBER: US/09/914,220
 10 <141> CURRENT FILING DATE: 2001-08-22
 12 <150> PRIOR APPLICATION NUMBER: DE 199 07 598.0
 13 <151> PRIOR FILING DATE: 1999-02-22
 15 <160> NUMBER OF SEQ ID NOS: 8
 17 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

309 <210> SEQ ID NO: 7
 310 <211> LENGTH: 776
 311 <212> TYPE: DNA
 312 <213> ORGANISM: Zea mays
 314 <400> SEQUENCE: 7
 315 tttttttttt tttttccccg tagcaacagt attattacta gcataatcta aatatgaaag 60
 316 ctgcaatata caatggcata aaaggccctt tgagctccag ttgaaagact gtatgaaact 120
 317 atggcataat agtgaacaac atcgtataga gtgcataaca actaattgat ccggaccggc 180
 318 cgacagttct acagaaaatt caacactcct tataatacaa gggttggtcaa ttaggccacc 240
 319 agttctacac aattttctgg taaattatcc tactcgttct tccgtttgaa catcccagcc 300
 320 agataaagga taaatgacac cagccactgc cagaacacaa cgaggactct tgccttcttc 360
 321 gggttcgctt caggacttgg cccaaagaga cctttgtaga gctccttctg cttctggtat 420
 E--> 322 agggcctttn) cttgttccgc gagcaaacgg agctcccga tgccttctt gttcttctggg 480
 323 gactacttct tcgctttgag gaaatcttcc ctgcgtgatt ctgtctggcc aagttcagat 540
 324 ttagcttttc ctgcctgaa cagcgctttg acattacttt catcttctgt caaaacaatg 600
 325 ctacactgcg caatagcttc atcgaatctc ttagtttga tcaggcatgc ggccatattg 660
 326 agatggcatg gatttttcac agccaaggcc atgtctctgt actttccaaa taattgaaac 720
 327 atgaaatcat ctcccatgta tgcaatcgcc atttcatatt gctgcatggc ctcttc 776
 330 <210> SEQ ID NO: 8
 331 <211> LENGTH: 168
 332 <212> TYPE: PRT
 333 <213> ORGANISM: Zea mays
 335 <400> SEQUENCE: 8
 336 Glu Glu Ala Met Gln Gln Tyr Glu Met Ala Ile Ala Tyr Met Gly Asp
 337 1 5 10 15
 339 Asp Phe Met Phe Gln Leu Phe Gly Lys Tyr Arg Asp Met Ala Leu Ala
 340 20 25 30
 342 Val Lys Asn Pro Cys His Leu Asn Met Ala Ala Cys Leu Ile Lys Leu
 343 35 40 45
 345 Lys Arg Phe Asp Glu Ala Ile Ala Gln Cys Ser Ile Val Leu Thr Glu
 346 50 55 60
 348 Asp Glu Ser Asn Val Lys Ala Leu Phe Arg Arg Gly Lys Ala Lys Ser
 349 65 70 75 80
 351 Glu Leu Gly Gln Thr Glu Ser Ala Arg Glu Asp Phe Leu Lys Ala Lys

> see
 item 9
 in Error
 summary
 sheet

DATE: 09/14/2001

TIME: 10:39:35

Input Set : A:\Debelseq.txt

Output Set: N:\CRF3\09142001\I914220.raw

```

      352              85          90             95
E--> 354 Lys Tyr Ser Pro Glu Xaa Lys Glu Ile Ile Arg Glu Leu Arg Leu Leu
      355              100         105            110
E--> 357 Ala Glu Gln Xaa Lys Ala Leu Tyr Gln Lys Gln Lys Glu Leu Tyr Lys
      358              115           120            125
      360 Gly Leu Phe Gly Pro Ser Pro Glu Ala Lys Pro Lys Lys Ala Lys Tyr
      361              130           135            140
      363 Leu Val Val Phe Trp Gln Trp Leu Val Ser Phe Ile Leu Tyr Leu Ala
      364 145              150            155            160
      366 Gly Met Phe Lys Arg Lys Asn Glu
      367              165

```

Item 9

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/914,220
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5' amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <u> </u> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	